

# Resource Summary Report

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## SwissRegulon

RRID:SCR\_005333

Type: Tool

### Proper Citation

SwissRegulon (RRID:SCR\_005333)

### Resource Information

**URL:** <http://swissregulon.unibas.ch/cgi/sr/swissregulon>

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**Description:** A database of genome-wide annotations of regulatory sites. The predictions are based on Bayesian probabilistic analysis of a combination of input information including: \* Experimentally determined binding sites reported in the literature. \* Known sequence-specificities of transcription factors. \* ChIP-chip and ChIP-seq data. \* Alignments of orthologous non-coding regions. Predictions were made using the PhyloGibbs, MotEvo, IRUS and ISMARA algorithms developed in their group, depending on the data available for each organism. Annotations can be viewed in a Gbrowse genome browser and can also be downloaded in flat file format.

**Abbreviations:** SwissRegulon

**Synonyms:** SwissRegulon Database

**Resource Type:** data or information resource, database

**Defining Citation:** [PMID:23180783](#), [PMID:17130146](#)

**Keywords:** genome, binding site, transcription factor, genome-wide annotation, annotation, chip-chip, chip-seq, non-coding region, promoter, motif, transcript, regulatory motif, genome browser, FASEB list

**Availability:** Acknowledgement requested

**Resource Name:** SwissRegulon

**Resource ID:** SCR\_005333

**Alternate IDs:** nif-0000-03524, OMICS\_00543

**Record Creation Time:** 20220129T080229+0000

## Ratings and Alerts

No rating or validation information has been found for SwissRegulon.

No alerts have been found for SwissRegulon.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 46 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [SPARC SAWG](#) .

Bhardwaj V, et al. (2026) Single-cell co-mapping reveals relationship between chromatin state and gene expression in early zebrafish development. eLife, 15.

Bahiri Elitzur S, et al. (2026) Design of bacterial DNT sensors based on computational models. Nucleic acids research, 54(1).

Ji L, et al. (2025) Identification of Schizophrenia-Risk Regulatory Variant rs1399178 in the Non-coding Region With Its Impact on NRF1 Binding. CNS neuroscience & therapeutics, 31(3), e70275.

Williquett J, et al. (2024) AMPK-SP1-Guided Dynein Expression Represents a New Energy-Responsive Mechanism and Therapeutic Target for Diabetic Nephropathy. Kidney360, 5(4), 538.

Ren X, et al. (2023) High throughput PRIME editing screens identify functional DNA variants in the human genome. bioRxiv : the preprint server for biology.

Pastore SF, et al. (2023) Neuronal transcription of autism gene PTCHD1 is regulated by a conserved downstream enhancer sequence. Scientific reports, 13(1), 20391.

Chen SA, et al. (2023) Gene-by-environment interactions are pervasive among natural genetic variants. Cell genomics, 3(4), 100273.

Liu D, et al. (2022) circKCNN2 suppresses the recurrence of hepatocellular carcinoma at least partially via regulating miR-520c-3p/methyl-DNA-binding domain protein 2 axis. Clinical and translational medicine, 12(1), e662.

Ajore R, et al. (2022) Functional dissection of inherited non-coding variation influencing multiple myeloma risk. Nature communications, 13(1), 151.

Cheng X, et al. (2022) Identification of potential functional variants and genes at 18q21.1 associated with the carcinogenesis of colorectal cancer. PLoS genetics, 18(2), e1010050.

Freddolino PL, et al. (2021) Dynamic landscape of protein occupancy across the Escherichia coli chromosome. PLoS biology, 19(6), e3001306.

Kang HG, et al. (2021) Genetic variants in histone modification regions are associated with the prognosis of lung adenocarcinoma. Scientific reports, 11(1), 21520.

Duran-Lozano L, et al. (2021) Germline variants at SOHLH2 influence multiple myeloma risk. Blood cancer journal, 11(4), 76.

Morello G, et al. (2021) Transcriptional Profiles of Cell Fate Transitions Reveal Early Drivers of Neuronal Apoptosis and Survival. Cells, 10(11).

Ducoli L, et al. (2021) LETR1 is a lymphatic endothelial-specific lncRNA governing cell proliferation and migration through KLF4 and SEMA3C. Nature communications, 12(1), 925.

Greulich F, et al. (2021) The glucocorticoid receptor recruits the COMPASS complex to regulate inflammatory transcription at macrophage enhancers. Cell reports, 34(6), 108742.

Yang W, et al. (2019) Three novel genetic variants in NRF2 signaling pathway genes are associated with pancreatic cancer risk. Cancer science, 110(6), 2022.

Li S, et al. (2019) Stable enhancers are active in development, and fragile enhancers are associated with evolutionary adaptation. Genome biology, 20(1), 140.

Franz O, et al. (2019) PanglaoDB: a web server for exploration of mouse and human single-cell RNA sequencing data. Database : the journal of biological databases and curation, 2019.

Weger BD, et al. (2019) The Mouse Microbiome Is Required for Sex-Specific Diurnal Rhythms of Gene Expression and Metabolism. Cell metabolism, 29(2), 362.